

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	5108	cleaning near4 detergent	USPAT	OR	OFF	2005/05/05 20:14
L2	58	cleaning near4 cellulase	USPAT	OR	OFF	2005/05/05 20:14
L3	36	L1 and L2 and cellulose	USPAT	OR	OFF	2005/05/05 20:14
L4	9	L3 and (cellulose adj binding adj domain)	USPAT	OR	OFF	2005/05/05 20:14
L5	1	L4 and thermostable	USPAT	OR	OFF	2005/05/05 20:14
L6	11	L3 and thermostable	USPAT	OR	OFF	2005/05/05 20:15
L7	1	l6 and cbd	USPAT	OR	OFF	2005/05/05 20:15



PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Features: SNP CDD MGC HPRD STS

Item 1 - 7 of 7

1: [P54583](#). Reports Endoglucanase E1 ...[gi:1708075]

[BLINK](#),
[Domains](#),
[Links](#)

LOCUS P54583 562 aa linear BCT 01-MAY-
 DEFINITION Endoglucanase E1 precursor (Endo-1,4-beta-glucanase E1) (Cellul E1) (Endocellulase E1).
 ACCESSION P54583
 VERSION P54583 GI:1708075
 DBSOURCE swissprot: locus GUN1_ACICE, accession [P54583](#);
 class: standard.
 created: Oct 1, 1996.
 sequence updated: Oct 1, 1996.
 annotation updated: May 1, 2005.
 xrefs: [U33212.1](#), [AAA75477.1](#), [1C0DA](#), [1C0DB](#), [1ECEA](#), [1ECEB](#)
 xrefs (non-sequence databases): InterProIPR001919,
 InterProIPR008965, InterProIPR001547, PfamPF00553, PfamPF00150,
 SMARTSM00637, PROSITEPS00659
 KEYWORDS 3D-structure; Carbohydrate metabolism; Cellulose degradation;
 Glycosidase; Hydrolase; Polysaccharide degradation; Signal.
 SOURCE Acidothermus cellulolyticus
 ORGANISM [Acidothermus cellulolyticus](#)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Frankineae; Acidothermaceae; Acidothermus.
 REFERENCE 1 (residues 1 to 562)
 AUTHORS Laymon,R.A., Himmel,M.E. and Thomas,S.R.
 TITLE Direct Submission
 JOURNAL Submitted (??-AUG-1995)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=ATCC 43068 / 11B
 REFERENCE 2 (residues 1 to 562)
 AUTHORS Sakon,J., Adney,W.S., Himmel,M.E., Thomas,S.R. and Karplus,P.A.
 TITLE Crystal structure of thermostable family 5 endocellulase E1 fro
 Acidothermus cellulolyticus in complex with cellobetraose
 JOURNAL Biochemistry 35 (33), 10648-10660 (1996)
 PUBMED [8718854](#)
 REMARK X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 42-398.
 COMMENT [FUNCTION] Has a very high specific activity on

carboxymethylcellulose.
[CATALYTIC ACTIVITY] Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.
[BIOPHYSICOCHEMICAL PROPERTIES] Temperature dependence: Optimum temperature is 81 degrees Celsius. Thermostable.
[SIMILARITY] Belongs to the glycosyl hydrolase 5 (cellulase A) family.
[SIMILARITY] Contains 1 CBM2 (carbohydrate binding type-2) domain

FEATURES

source

Location/Qualifiers

1..562

/organism="Acidothermus cellulolyticus"
/db_xref="taxon:28049"Protein

1..562

/product="Endoglucanase E1 precursor"
/EC_number="3.2.1.4"Region

1..41

/region_name="Signal"
/evidence=experimentalRegion

42..562

/region_name="Mature chain"
/note="Endoglucanase E1."

/evidence=experimental

Region

42..400

/region_name="Domain"
/note="Catalytic."
/evidence=experimentalRegion

48..50

/region_name="Beta-strand region"
/evidence=experimentalRegion

51..52

/region_name="Hydrogen bonded turn"
/evidence=experimentalRegion

53..55

/region_name="Beta-strand region"
/evidence=experimentalRegion

57..58

/region_name="Hydrogen bonded turn"
/evidence=experimentalRegion

61..62

/region_name="Beta-strand region"
/evidence=experimentalRegion

65..68

/region_name="Beta-strand region"
/evidence=experimentalRegion

72

/region_name="Beta-strand region"
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73

/region_name="Hydrogen bonded turn"
/evidence=experimental

Bond bond(75,161)
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/evidence=experimental
Region 75..76
/region_name="Hydrogen bonded turn"
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Region 80..84
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Region 87..96
/region_name="Helical region"
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Region 97..98
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 101..107
/region_name="Beta-strand region"
/evidence=experimental
Region 108..111
/region_name="Helical region"
/evidence=experimental
Region 113..114
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Region 127..129
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/evidence=experimental
Region 130..131
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/evidence=experimental
Region 134..147
/region_name="Helical region"
/evidence=experimental
Region 148..149
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 151..158
/region_name="Beta-strand region"
/evidence=experimental
Region 160
/region_name="Beta-strand region"
/evidence=experimental
Region 161..162
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 163
/region_name="Beta-strand region"
/evidence=experimental
Region 175..188
/region_name="Helical region"

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Region          189..191
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Region          193..194
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                  /evidence=experimental
Region          195..199
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                  /evidence=experimental
Site            203
                  /site_type="active"
                  /note="Proton donor."
                  /evidence=experimental
Region          206..207
                  /region_name="Hydrogen bonded turn"
                  /evidence=experimental
Bond            bond(209,212)
                  /bond_type="disulfide"
                  /evidence=experimental
Region          209
                  /region_name="Beta-strand region"
                  /evidence=experimental
Region          215..217
                  /region_name="Hydrogen bonded turn"
                  /evidence=experimental
Region          218
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                  /evidence=experimental
Region          219..230
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                  /evidence=experimental
Region          231..233
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Region          235..236
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                  /evidence=experimental
Region          244
                  /region_name="Beta-strand region"
                  /evidence=experimental
Region          246..247
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                  /evidence=experimental
Region          248..249
                  /region_name="Hydrogen bonded turn"
                  /evidence=experimental
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/evidence=experimental
Region 254..255
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 257
/region_name="Beta-strand region"
/evidence=experimental
Region 259..263
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 274..279
/region_name="Beta-strand region"
/evidence=experimental
Region 283..285
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 289..292
/region_name="Helical region"
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Region 294..299
/region_name="Hydrogen bonded turn"
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Region 300..307
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Region 309..313
/region_name="Helical region"
/evidence=experimental
Region 314..315
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 319..323
/region_name="Beta-strand region"
/evidence=experimental
Site 323
/site_type="active"
/note="Nucleophile."
/evidence=experimental
Region 331..343
/region_name="Helical region"
/evidence=experimental
Region 344
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 347..350

Region

/region_name="Helical region"
/evidence=experimental
351..352

Region

/region_name="Hydrogen bonded turn"
/evidence=experimental
356..359

Region

/region_name="Beta-strand region"
/evidence=experimental
367..369

Region

/region_name="Hydrogen bonded turn"
/evidence=experimental
373

Region

/region_name="Beta-strand region"
/evidence=experimental
375..376

Region

/region_name="Hydrogen bonded turn"
/evidence=experimental
380

Region

/region_name="Beta-strand region"
/evidence=experimental
382..387

Region

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/evidence=experimental
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Region

/region_name="Hydrogen bonded turn"
/evidence=experimental
389..391

Region

/region_name="Helical region"
/evidence=experimental
401..461

Region

/region_name="Domain"
/note="Pro/Ser/Thr-rich (linker)."
/evidence=experimental
462..562

Region

/region_name="Domain"
/note="CBM2."
/evidence=experimental

ORIGIN

1 mpralrrvpg srvmrlrvgvv vavlavala anlavprpar aagggywhts greildannv
61 pvriaginwf gfetcnyvvh glwsrdyrsm ldqikslgyn tirlpysddi lkpgtmpnsi
121 nfyqmnnqdlq gltslqvmdk ivayaggqigl riildrhrpd csgqsalwyt ssvseatwis
181 dlqalaqryk gnptvvvgfdl hnephdpacw gcgdpssidwr laaeragnav lsvnpnllif
241 vegvqsyngd sywwgggnlqg agqypvvlnv pnrlvysahd yatsvypqtw fsdptfpnnm
301 pgiwnknwgy lfnqniaspvw lgefttqls ttdqtwlktl vqylrptaqy gadsfqwtfw
361 swnpdsgdtg gilkddwqtv dtvkdgylap ikssifdpvg asaspssqps psvspspsp
421 psasrtptpt ptptasptpt ltptatptpt asptpsptaa sgarcctasyq vnsdwngngft
481 vtvavtnsgs vatktwtvsw tfgggnqtitn swnaavtqng qsvtarnmsy nnviqpgqnt
541 tfgfqaqytg snaaptvaca as

11

□ 2: CAD42489. Reports unnamed protein p...[gi:21900783]

BLink, Links

LOCUS CAD42489 562 aa linear BCT 16-JUL-
 DEFINITION unnamed protein product [Acidothermus cellulolyticus].
 ACCESSION CAD42489
 VERSION CAD42489.1 GI:21900783
 DBSOURCE embl accession AX467594.1
 KEYWORDS .
 SOURCE Acidothermus cellulolyticus
 ORGANISM Acidothermus cellulolyticus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Frankineae; Acidothermaceae; Acidothermus.
 REFERENCE 1
 AUTHORS Sticklen,M.B., Dale,B.E. and Maqbool,S.
 TITLE Transgenic plants containing ligninase and cellulase which degr
 lignin and cellulose to fermentable sugars
 JOURNAL Patent: WO 0234926-A 02-MAY-2002;
 MICHIGAN STATE UNIVERSITY (US)
 FEATURES Location/Qualifiers
 · source 1..562
 /organism="Acidothermus cellulolyticus"
 /db_xref="taxon:28049"
Protein 1..562
 /name="unnamed protein product"
CDS 1..562
 /coded_by="AX467594.1:824..2512"
 /note="E I beta-1,4-endoglucanase precursor"
 /transl_table=11

ORIGIN

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1 mpralrrvpg srvmrlvgvv vavlalvaal anlavprpar aagggywhts greildannv
 61 pvriaginwf gfetcnyvh glwsrdyrsrn ldqikslgyn tirlpysddi lkpgtjmpnsi
121 nfyqmnnqdlq gltslqvmdk ivayaggqigl riildrhrpd csgqsalwyt ssvseatwls
181 dlqalaqryk gnptvvgfld hnephdpacw gcgdpssidwr laaeragnav lsvnpnllif
241 vegvqsyngd sywwggnlqg agqypvvlv pnrlvysahd yatsvypqtw fsdptfpnnm
301 pgiwnknwgy lfnqnpiapvw lgefgttlqs ttdqtwlktl vqylrptaqy gadsfqwtfw
361 swnpdsgdtg gilkddwqtv dtvkdgylap ikssifdpvg asaspssqps psvspspsp
421 psasrtptpt ptptasptpt ltptatptpt asptpsptaa sgarctasyq vnsdwgnqft
481 vtvavtnsgs vatktwtvsw tfgggnqtin swnaavtqng qsvtarnmsy nnviqpgqnt
541 tfgfqasytg snaaptvaca as
//
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□ 3: 1C0D_B. Reports Chain B, Endocell...[gi:5821930]BLink,
Domains,
Links

LOCUS 1C0D_B 358 aa linear BCT 15-JUL-
 DEFINITION Chain B, Endocellulase E1 From Acidothermus Cellulolyticus Mut
 Y245g.
 ACCESSION 1C0D_B

VERSION 1C0D_B GI:5821930
DBSOURCE pdb: molecule 1C0D, chain 66, release Jul 15, 1999;
deposition: Jul 15, 1999;
class: Hydrolase;
source: Mol_id: 1; Organism_scientific: Acidothermus
Cellulolyticus; Organism_common: Thermophilic Bacterium From Th
Yellowstone National Park; Expression_system: Escherichia Coli;
Expression_system_common: Bacteria;
Exp. method: X-Ray Diffraction.

KEYWORDS .

SOURCE Acidothermus cellulolyticus

ORGANISM Acidothermus cellulolyticus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Frankineae; Acidothermaceae; Acidothermus.

REFERENCE 1 (residues 1 to 358)

AUTHORS Mccarley, J.R., Lovett, R.M., Sakon, J., Himmel, M.E. and Baker, J.O

TITLE Catalytically Enhanced Endocellulase E1 From Acidothermus
Cellulolyticus

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 358)

AUTHORS Mccarley, J.R., Lovett, R.M., Sakon, J., Himmel, M.E. and Baker, J.O

TITLE Direct Submission

JOURNAL Submitted (15-JUL-1999)

COMMENT Revision History:
JUL 23 99 Initial Entry.

FEATURES Location/Qualifiers

source 1..358
/organism="Acidothermus cellulolyticus"
/db_xref="taxon:28049"

SecStr 5..10
/sec_str_type="sheet"
/note="strand 16"

SecStr 11..16
/sec_str_type="sheet"
/note="strand 17"

SecStr 23..29
/sec_str_type="sheet"
/note="strand 18"

Bond bond(34,120)
/bond_type="disulfide"

SecStr 46..56
/sec_str_type="helix"
/note="helix 7"

SecStr 59..65
/sec_str_type="sheet"
/note="strand 19"

SecStr 93..106
/sec_str_type="helix"
/note="helix 8"

SecStr 107..115

/sec_str_type="sheet"
 /note="strand 20"
SecStr 134..148
 /sec_str_type="helix"
 /note="helix 9"
SecStr 155..159
 /sec_str_type="sheet"
 /note="strand 21"
SecStr 167..170
 /sec_str_type="sheet"
 /note="strand 22"
Bond bond(168,171)
 /bond_type="disulfide"
SecStr 176..179
 /sec_str_type="sheet"
 /note="strand 23"
SecStr 180..192
 /sec_str_type="helix"
 /note="helix 10"
SecStr 196..202
 /sec_str_type="sheet"
 /note="strand 24"
SecStr 204..207
 /sec_str_type="sheet"
 /note="strand 25"
SecStr 208..211
 /sec_str_type="sheet"
 /note="strand 26"
SecStr 232..240
 /sec_str_type="sheet"
 /note="strand 27"
SecStr 259..266
 /sec_str_type="helix"
 /note="helix 11"
SecStr 277..284
 /sec_str_type="sheet"
 /note="strand 28"
SecStr 290..302
 /sec_str_type="helix"
 /note="helix 12"
SecStr 314..319
 /sec_str_type="sheet"
 /note="strand 29"
SecStr 355..358
 /sec_str_type="sheet"
 /note="strand 30"

ORIGIN

1 aggywhtsg reildannvp vriaginwfg fetcnyvvhg lwsrdyrsml dqikslgynt
61 irlpysddil kpgtmpnsin fyqmnqdlqg ltslqvmdki vayaggiglr iildrhrpd
121 sgqsalwyts svseatwisd lqalaqrykg nptvvgfdlh nephdpacwg cgdpsidwrl

181 aaeragnav1 svnpnllifv evqsyngds ywwggnlqga qqypvvlnvp nrlvysahdy
 241 atsvgpqtwf sdptfpnnmp giwnknwgyl fnqniapwl gefgttlqst tdqtwlktlv
 301 qylrptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtvd tdkdgylapi kssifdpv
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4: 1C0DA. Reports Chain A, Endocell...[gi:5821929]

BLINK,
Domains,
Links

LOCUS 1C0D_A 358 aa linear BCT 15-JUL-
 DEFINITION Chain A, Endocellulase E1 From Acidothermus Cellulolyticus Mutant Y245g.
 ACCESSION 1C0D_A
 VERSION 1C0D_A GI:5821929
 DBSOURCE pdb: molecule 1C0D, chain 65, release Jul 15, 1999;
 deposition: Jul 15, 1999;
 class: Hydrolase;
 source: Mol_id: 1; Organism_scientific: Acidothermus Cellulolyticus; Organism_common: Thermophilic Bacterium From The Yellowstone National Park; Expression_system: Escherichia Coli; Expression_system_common: Bacteria;
 Exp. method: X-Ray Diffraction.
 KEYWORDS .
 SOURCE Acidothermus cellulolyticus
 ORGANISM Acidothermus cellulolyticus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Frankineae; Acidothermaceae; Acidothermus.
 REFERENCE 1 (residues 1 to 358)
 AUTHORS Mccarley, J.R., Lovett, R.M., Sakon, J., Himmel, M.E. and Baker, J.O.
 TITLE Catalytically Enhanced Endocellulase E1 From Acidothermus Cellulolyticus
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 358)
 AUTHORS Mccarley, J.R., Lovett, R.M., Sakon, J., Himmel, M.E. and Baker, J.O.
 TITLE Direct Submission
 JOURNAL Submitted (15-JUL-1999)
 COMMENT Revision History:
 JUL 23 99 Initial Entry.
 FEATURES Location/Qualifiers
 source 1..358
 /organism="Acidothermus cellulolyticus"
 /db_xref="taxon:28049"
SecStr 5..10
 /sec_str_type="sheet"
 /note="strand 1"
SecStr 11..16
 /sec_str_type="sheet"
 /note="strand 2"
SecStr 23..29

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        /note="strand 3"
Bond          bond(34,120)
                    /bond_type="disulfide"
SecStr        46..56
                    /sec_str_type="helix"
                    /note="helix 1"
SecStr        59..65
                    /sec_str_type="sheet"
                    /note="strand 4"
SecStr        93..106
                    /sec_str_type="helix"
                    /note="helix 2"
SecStr        107..115
                    /sec_str_type="sheet"
                    /note="strand 5"
SecStr        134..148
                    /sec_str_type="helix"
                    /note="helix 3"
SecStr        155..159
                    /sec_str_type="sheet"
                    /note="strand 6"
SecStr        167..170
                    /sec_str_type="sheet"
                    /note="strand 7"
Bond          bond(168,171)
                    /bond_type="disulfide"
SecStr        176..179
                    /sec_str_type="sheet"
                    /note="strand 8"
SecStr        180..192
                    /sec_str_type="helix"
                    /note="helix 4"
SecStr        196..202
                    /sec_str_type="sheet"
                    /note="strand 9"
SecStr        204..207
                    /sec_str_type="sheet"
                    /note="strand 10"
SecStr        208..211
                    /sec_str_type="sheet"
                    /note="strand 11"
SecStr        232..240
                    /sec_str_type="sheet"
                    /note="strand 12"
SecStr        259..266
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                    /note="helix 5"
SecStr        277..284
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SecStr      290..302
        /sec_str_type="helix"
        /note="helix 6"
SecStr      314..319
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        /note="strand 14"
SecStr      355..358
        /sec_str_type="sheet"
        /note="strand 15"

ORIGIN
1 aggywhtsg reildannvp vriaginwfg fetcnvvvhg lwsrdyrsml dqikslgynt
61 irlpysddil kpgtmpnsin fyqmnqdlqq ltslqvmdki vayaggiglr iildrhrpdc
121 sgqsalwyts svseatwisd lqalaqrykg nptvvgfdlh nephdpacwg cgdpsidwrl
181 aaeragnavl svnpnllifv evgqsyngds ywwggnlqga gqypvvlnvp nrlvysahdy
241 atsvgpqtwf sdptfpnnmp giwnknwgyl fnqniapvw1 gefgttlqst tdqtwlktlv
301 qylrptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtvd tdkdgylapi kssifdpv
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5: 1ECEB. Reports Chain B, Acidotherm...[gi:1827682]

BLink,
Domains,
Links

LOCUS	1ECE_B	358 aa	linear	BCT 04-APR-
DEFINITION	Chain B, Acidothermus Cellulolyticus Endocellulase E1 Catalytic Domain In Complex With A Cellotetraose.			
ACCESSION	1ECE_B			
VERSION	1ECE_B GI:1827682			
DBSOURCE	pdb: molecule 1ECE, chain 66, release Apr 4, 1996; deposition: Apr 4, 1996; class: Glycosyl Hydrolase; source: Mol_id: 1; Organism_scientific: Acidothermus Cellulolyticus; Expression_system: Streptomyces Lividans; Expression_system_strain: Tk24; Expression_system_plasmid: Pij7 Expression_system_gene: Pvu I Fragment Of A. Cellulolyticus Gen Dna Carrying Native E1 Gene; Exp. method: X-Ray Diffraction.			
KEYWORDS	.			
SOURCE	Acidothermus cellulolyticus			
ORGANISM	<u>Acidothermus cellulolyticus</u> Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Frankineae; Acidothermaceae; Acidothermus.			
REFERENCE	1 (residues 1 to 358)			
AUTHORS	Sakon,J., Thomas,S.R., Himmel,M.E. and Karplus,P.A.			
TITLE	Direct Submission			
JOURNAL	Submitted (04-APR-1996)			
COMMENT	Revision History: OCT 14 96 Initial Entry.			
FEATURES	Location/Qualifiers			

source 1..358
/organism="Acidothermus cellulolyticus"
/db_xref="taxon:28049"
SecStr 5..10
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/note="strand 15"
SecStr 11..16
/sec_str_type="sheet"
/note="strand 16"
SecStr 23..29
/sec_str_type="sheet"
/note="strand 17"
Bond bond(34,120)
/bond_type="disulfide"
SecStr 46..56
/sec_str_type="helix"
/note="helix 7"
SecStr 59..65
/sec_str_type="sheet"
/note="strand 18"
SecStr 93..107
/sec_str_type="helix"
/note="helix 8"
SecStr 109..115
/sec_str_type="sheet"
/note="strand 19"
SecStr 134..148
/sec_str_type="helix"
/note="helix 9"
SecStr 155..159
/sec_str_type="sheet"
/note="strand 20"
SecStr 167..170
/sec_str_type="sheet"
/note="strand 21"
Bond bond(168,171)
/bond_type="disulfide"
SecStr 176..179
/sec_str_type="sheet"
/note="strand 22"
SecStr 180..192
/sec_str_type="helix"
/note="helix 10"
SecStr 196..202
/sec_str_type="sheet"
/note="strand 23"
SecStr 204..207
/sec_str_type="sheet"
/note="strand 24"
SecStr 208..211

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        /sec_str_type="sheet"
        /note="strand 25"
SecStr    232..238
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        /note="strand 26"
SecStr    259..266
        /sec_str_type="helix"
        /note="helix 11"
SecStr    277..282
        /sec_str_type="sheet"
        /note="strand 27"
SecStr    290..302
        /sec_str_type="helix"
        /note="helix 12"
SecStr    314..319
        /sec_str_type="sheet"
        /note="strand 28"

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ORIGIN

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121 sgqsalwyts svseatwisd lqalaqrykg nptvvgfldh nephdpacwg cgdpsidwrl
181 aaeragnavl svnpnllifv evqsyngds ywwggnlqga gqypvvlnvp nrlvysahdy
241 atsvypqtwf sdptfpnnmp giwnknwgyl fnqniapvw1 gefgttlqst tdqtwlktlv
301 qylrptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtvd tvkdgy1api kssifdpv
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□ 6: [1ECE_A](#). Reports Chain A, Acidotherm...[gi:1827681]

BLink,
Domains,
Links

LOCUS	1ECE_A	358 aa	linear	BCT 04-APR-
DEFINITION	Chain A, Acidothermus Cellulolyticus Endocellulase E1 Catalytic Domain In Complex With A Cellotetraose.			
ACCESSION	1ECE_A			
VERSION	1ECE_A GI:1827681			
DBSOURCE	pdb: molecule 1ECE, chain 65, release Apr 4, 1996; deposition: Apr 4, 1996; class: Glycosyl Hydrolase; source: Mol_id: 1; Organism_scientific: Acidothermus Cellulolyticus; Expression_system: Streptomyces Lividans; Expression_system_strain: Tk24; Expression_system_plasmid: Pij7 Expression_system_gene: Pvu I Fragment Of A. Cellulolyticus Gen Dna Carrying Native E1 Gene; Exp. method: X-Ray Diffraction.			
KEYWORDS	.			
SOURCE	Acidothermus cellulolyticus			
ORGANISM	<u>Acidothermus cellulolyticus</u> Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Frankineae; Acidothermaceae; Acidothermus.			

REFERENCE 1 (residues 1 to 358)
AUTHORS Sakon,J., Thomas,S.R., Himmel,M.E. and Karplus,P.A.
TITLE Direct Submission
JOURNAL Submitted (04-APR-1996)
COMMENT Revision History:
OCT 14 96 Initial Entry.
FEATURES Location/Qualifiers
source 1..358
/organism="Acidothermus cellulolyticus"
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/note="strand 1"
SecStr 11..16
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/note="strand 2"
SecStr 23..29
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/note="strand 3"
Bond bond(34,120)
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SecStr 46..56
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SecStr 59..65
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/note="strand 4"
SecStr 93..107
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SecStr 109..115
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/note="strand 5"
SecStr 134..148
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/note="helix 3"
SecStr 155..159
/sec_str_type="sheet"
/note="strand 6"
SecStr 167..170
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Bond bond(168,171)
/bond_type="disulfide"
SecStr 176..179
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/note="strand 8"
SecStr 180..192
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/note="helix 4"

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SecStr          232..238
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SecStr          259..266
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SecStr          277..282
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                 /note="strand 13"
SecStr          290..302
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SecStr          314..319
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ORIGIN

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121 sgqsalwyts svseatwisd lqalaqrykg nptvvvgfdlh nephdpacwg cgdpsidwrl
181 aaeragnavl svnpnllifv egvqsyngds ywwggnlqga gqypvvlnvp nrlvysahdy
241 atsvypqtwf sdptfpnnmp giwnknwgyl fnqniapvw1 gefgttlqst tdqtwlktlv
301 qylrpptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtvd tvkdgylap1 kssifdpv
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7: [AAA75477](#). Reports E I beta-1,4-endo...[gi:988300]

[BLink](#),
[Domains](#),
[Links](#)

LOCUS	AAA75477	562 aa	linear	BCT 19-SEP-
DEFINITION	E I beta-1,4-endoglucanase precursor.			
ACCESSION	AAA75477			
VERSION	AAA75477.1 GI:988300			
DBSOURCE	locus ACU33212 accession U33212.1			
KEYWORDS	.			
SOURCE	Acidothermus cellulolyticus			
ORGANISM	<u>Acidothermus cellulolyticus</u>			
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
	Frankineae; Acidothermaceae; Acidothermus.			
REFERENCE	1 (residues 1 to 562)			
AUTHORS	Laymon,R.A., Himmel,M.E. and Thomas,S.R.			

TITLE Direct Submission
JOURNAL Submitted (04-AUG-1995) Steven R. Thomas, Applied Biological Sciences, National Renewable Energy Laboratory, 1617 Cole Blvd. Golden, CO 80401, USA
COMMENT Method: conceptual translation.
FEATURES
 source Location/Qualifiers
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 Protein 1..562
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 sig peptide 1..41
 mat peptide 42..562
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 /transl_table=11
ORIGIN
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 61 pvriaginwf gfetcnyvvh glwsrdyrsm ldqikslgyn tirlpysddi lkpgtmpnsi
 121 nfyqmnnqdlq gltslqvmdk ivayaggqigl riildrhrpd csgqsalwyt ssvseatwis
 181 dlqalaqryk gnptvvvgfdl hnephdpacw gcgdpsidwr laaeragnav lsvnpnllif
 241 vegvqsyngd sywwgggnlqg agqypvvlnv pnrlvysahd yatsvypqtw fsdptfpnnm
 301 pgiwnknwgy lfnqniaspvw lgefgttlqs ttdqtwlktl vqylrptaqy gadsfqwtfw
 361 swnpdsgdtg gilkddwqtv dtvkdgylap ikssifdpvg asaspssqps psvspspsp
 421 psasrtptpt ptptasptpt ltptatptpt asptpsptaa sgarctasyq vnsdwgngft
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 541 tfgfqasatyg snaaptvaca as
//

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